Genetic diversity of Pantoea stewartii subspecies stewartii causing jackfruit-bronzing disease in Malaysia

ABSTRACT

Jackfruit-bronzing is caused by bacteria Pantoea stewartii subspecies stewartii (P. stewartii subsp. stewartii), showing symptoms of yellowish-orange to reddish discolouration and rusty specks on pulps and rags of jackfruit. Twenty-eight pure bacterial strains were collected from four different jackfruit outbreak collection areas in Peninsular Malaysia (Jenderam, Maran, Muadzam Shah and Ipoh). Positive P. stewartii subsp. stewartii verification obtained in the study was based on the phenotypic, hypersensitivity, pathogenicity and molecular tests. Multilocus sequence analysis (MLSA) was performed using four housekeeping genes (gyrB, rpoB, atpD and infB) on all 28 bacterial strains. Single gyrB, rpoB, atpD and infB phylogenetic trees analyses revealed the bootstrap value of 99–100% between our bacterial strains with P. stewartii subsp. stewartii reference strains and P. stewartii subsp. indologenes reference strains. On the other hand, phylogenetic tree of the concatenated sequences of the four housekeeping genes revealed that our 28 bacterial strains were more closely related to P. stewartii subsp. stewartii (99% similarities) compared to its close relative P. stewartii subsp. indologenes, although sequence similarity between these two subspecies were up to 100%. All the strains collected from the four collection areas clustered together, pointing to no variation among the bacterial strains. This study improves our understanding and provided new insight on the genetic diversity of P. stewartii subsp. stewartii associated with jackfruit-bronzing in Malaysia.